SEQUENCE LISTING

<110> Jegla, Timothy James
ICAgen, Inc.

<120> Human HAC3

<130> 018512-002210US

<140> US 09/548,933
<141> 2000-04-13

<150> US 60/129,456
<151> 1999-04-15

<160> 16

<170> PatentIn Ver. 2.1

<210> 1
<211> 774
<212> PRT
<213> Homo sapiens

<220>
<223> human hyperpolarization-activated voltage-gated cation channel 3 (HAC3)

<400> 1

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Met Glu Ala Glu Gln Arg Pro Ala Ala Gly Ala Ser Glu Gly Ala Thr
 1               5                  10                  15

Pro Gly Leu Glu Ala Val Pro Pro Val Ala Pro Pro Pro Ala Thr Ala
            20                  25                  30

Ala Ser Gly Pro Ile Pro Lys Ser Gly Pro Glu Pro Lys Arg Arg His
        35                  40                  45

Leu Gly Thr Leu Leu Gln Pro Thr Val Asn Lys Phe Ser Leu Arg Val
    50                  55                  60

Phe Gly Ser His Lys Ala Val Glu Ile Glu Gln Glu Arg Val Lys Ser
65                  70                  75                  80

Ala Gly Ala Trp Ile Ile His Pro Tyr Ser Asp Phe Arg Phe Tyr Trp
                85                  90                  95

Asp Leu Ile Met Leu Leu Leu Met Val Gly Asn Leu Ile Val Leu Pro
            100                 105                 110

Val Gly Ile Thr Phe Phe Lys Glu Glu Asn Ser Pro Pro Trp Ile Val
        115                 120                 125

Phe Asn Val Leu Ser Asp Thr Phe Phe Leu Leu Asp Leu Val Leu Asn
    130                 135                 140

Phe Arg Thr Gly Ile Val Val Glu Glu Gly Ala Glu Ile Leu Leu Ala
145                 150                 155                 160

Pro Arg Ala Ile Arg Thr Arg Tyr Leu Arg Thr Trp Phe Leu Val Asp
                165                 170                 175
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Leu Ile Ser Ser Ile Pro Val Asp Tyr Ile Phe Leu Val Val Glu Leu
180 185 190

Glu Pro Arg Leu Asp Ala Glu Val Tyr Lys Thr Ala Arg Ala Leu Arg
195 200 205

Ile Val Arg Phe Thr Lys Ile Leu Ser Leu Leu Arg Leu Leu Arg Leu
210 215 220

Ser Arg Leu Ile Arg Tyr Ile His Gln Trp Glu Glu Ile Phe His Met
225 230 235 240

Thr Tyr Asp Leu Ala Ser Ala Val Val Arg Ile Phe Asn Leu Ile Gly
245 250 255

Met Met Leu Leu Leu Cys His Trp Asp Gly Cys Leu Gln Phe Leu Val
260 265 270

Pro Met Leu Gln Asp Phe Pro Pro Asp Cys Trp Val Ser Ile Asn His
275 280 285

Met Val Asn His Ser Trp Gly Arg Gln Tyr Ser His Ala Leu Phe Lys
290 295 300

Ala Met Ser His Met Leu Cys Ile Gly Tyr Gly Gln Gln Ala Pro Val
305 310 315 320

Gly Met Pro Asp Val Trp Leu Thr Met Leu Ser Met Ile Val Gly Ala
325 330 335

Thr Cys Tyr Ala Met Phe Ile Gly His Ala Thr Ala Leu Ile Gln Ser
340 345 350

Leu Asp Ser Ser Arg Arg Gln Tyr Gln Glu Lys Tyr Lys Gln Val Glu
355 360 365

Gln Tyr Met Ser Phe His Lys Leu Pro Ala Asp Thr Arg Gln Arg Ile
370 375 380

His Glu Tyr Tyr Glu His Arg Tyr Gln Gly Lys Met Phe Asp Glu Glu
385 390 395 400

Ser Ile Leu Gly Glu Leu Ser Glu Pro Leu Arg Glu Glu Ile Ile Asn
405 410 415

Phe Thr Cys Arg Gly Leu Val Ala His Met Pro Leu Phe Ala His Ala
420 425 430

Asp Pro Ser Phe Val Thr Ala Val Leu Thr Lys Leu Arg Phe Glu Val
435 440 445

Phe Gln Pro Gly Asp Leu Val Val Arg Glu Gly Ser Val Gly Arg Lys
450 455 460

Met Tyr Phe Ile Gln His Gly Leu Leu Ser Val Leu Ala Arg Gly Ala
465 470 475 480

Arg Asp Thr Arg Leu Thr Asp Gly Ser Tyr Phe Gly Glu Ile Cys Leu
485 490 495

Leu Thr Arg Gly Arg Arg Thr Ala Ser Val Arg Ala Asp Thr Tyr Cys
500 505 510

Arg Leu Tyr Ser Leu Ser Val Asp His Phe Asn Ala Val Leu Glu Glu
515 520 525

Phe Pro Met Met Arg Arg Ala Phe Glu Thr Val Ala Met Asp Arg Leu
530 535 540

Leu Arg Ile Gly Lys Lys Asn Ser Ile Leu Gln Arg Lys Arg Ser Glu
545 550 555 560

Pro Ser Pro Gly Ser Ser Gly Gly Ile Met Glu Gln His Leu Val Gln
565 570 575

His Asp Arg Asp Met Ala Arg Gly Val Arg Gly Arg Ala Pro Ser Thr
580 585 590

Gly Ala Gln Leu Ser Gly Lys Pro Val Leu Trp Glu Pro Leu Val His
595 600 605

Ala Pro Leu Gln Ala Ala Ala Val Thr Ser Asn Val Ala Ile Ala Leu
610 615 620

Thr His Gln Arg Gly Pro Leu Pro Leu Ser Pro Asp Ser Pro Ala Thr
625 630 635 640

Leu Leu Ala Arg Ser Ala Trp Arg Ser Ala Gly Ser Pro Ala Ser Pro
645 650 655

Leu Val Pro Val Arg Ala Gly Pro Trp Ala Ser Thr Ser Arg Leu Pro
660 665 670

Ala Pro Pro Ala Arg Thr Leu His Ala Ser Leu Ser Arg Ala Gly Arg
675 680 685

Ser Gln Val Ser Leu Leu Gly Pro Pro Pro Gly Gly Gly Gly Arg Arg
690 695 700

Leu Gly Pro Arg Gly Arg Pro Leu Ser Ala Ser Gln Pro Ser Leu Pro
705 710 715 720

Gln Arg Ala Thr Gly Asp Gly Ser Pro Gly Arg Lys Gly Ser Gly Ser
725 730 735

Glu Arg Leu Pro Pro Ser Gly Leu Leu Ala Lys Pro Pro Arg Thr Ala
740 745 750

Gln Pro Pro Arg Pro Pro Val Pro Glu Pro Ala Thr Pro Arg Gly Leu
755 760 765

Gln Leu Ser Ala Asn Met
770

<210> 2
<211> 2325
<212> DNA
<213> Homo sapiens

<220>
<223> human hyperpolarization-activated voltage-gated
cation channel 3 (HAC3)

<400> 2
atggaggcag agcagcggcc ggcggcgggg gccagcgaag gggcgacccc tggactggag 60
gcggtgcctc ccgttgctcc cccgcctgcg accgcggcct caggtccgat ccccaaatct 120
gggcctgagc ctaagaggag gcaccttggg acgctgctcc agcctacggt caacaagttc 180
tcccttcggg tgttcggcag ccacaaagca gtggaaatcg agcaggagcg ggtgaagtca 240
gcgggggcct ggatcatcca cccctacagc gacttccggt tttactggga cctgatcatg 300
ctgctgctga tggtggggaa cctcatcgtc ctgcctgtgg gcatcacctt cttcaaggag 360
gagaactccc cgccttggat cgtcttcaac gtattgtctg atactttctt cctactggat 420
ctggtgctca acttccgaac gggcatcgtg gtggaggagg gtgctgagat cctgctggca 480
ccgcgggcca tccgcacgcg ctacctgcgc acatggttcc tggttgacct catctcttct 540
atccctgtgg attacatctt cctagtggtg gagctggagc cacggttgga cgctgaggtc 600
tacaaaacgg cacgggccct acgcatcgtt cgcttcacca agatcctaag cctgctgagg 660
ctgctccgcc tctcccgcct catccgctac atacaccagt gggaggagat ctttcacatg 720
acctatgacc tggccagtgc tgtggttcgc atcttcaacc tcattgggat gatgctgctg 780
ctatgtcact gggatggctg tctgcagttc ctggtgccca tgctgcagga cttccctccc 840
gactgctggg tctccatcaa ccacatggtg aaccactcgt ggggccgcca gtattcccat 900
gccctgttca aggccatgag ccacatgctg tgcattggct atgggcagca ggcacctgta 960
ggcatgcccg acgtctggct caccatgctc agcatgatcg taggtgccac atgctacgcc 1020
atgttcatcg gccatgccac ggcactcatc cagtccctgg actcttcccg gcgtcagtac 1080
caggagaagt acaagcaggt ggagcagtac atgtccttcc acaagctgcc agcagacacg 1140
cggcagcgca tccacgagta ctatgagcac cgctaccagg gcaagatgtt cgatgaggaa 1200
agcatcctgg gcgagctgag cgagccgctt cgcgaggaga tcattaactt cacctgtcgg 1260
ggcctggtgg cccacatgcc gctgtttgcc catgccgacc ccagcttcgt cactgcagtt 1320
ctcaccaagc tgcgctttga ggtcttccag ccgggggatc tcgtggtgcg tgagggctcc 1380
gtggggagga agatgtactt catccagcat gggctgctca gtgtgctggc ccgcggcgcc 1440
cgggacacac gcctcaccga tggatcctac tttggggaga tctgcctgct aactaggggc 1500
cggcgcacag ccagtgttcg ggctgacacc tactgccgcc tttactcact cagcgtggac 1560
catttcaatg ctgtgcttga ggagttcccc atgatgcgcc gggcctttga gactgtggcc 1620
atggatcggc tgctccgcat cggcaagaag aattccatac tgcagcggaa gcgctccgag 1680
ccaagtccag gcagcagtgg tggcatcatg gagcagcact tggtgcaaca tgacagagac 1740
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gccattgccc tgactcatca gcggggcgct ctgcccctct cccctgactc tccagccacc 1920
ctccttgctc gctctgcttg gcgctcagca ggctctccag cttccccgct ggtgcccgtc 1980
cgagctggcc catgggcatc cacctcccgc ctgcccgccc cacctgcccg aaccctgcac 2040
gccagcctat cccgggcagg gcgctcccag gtctccctgc tgggtccccc tccaggagga 2100
ggtggacggc ggctaggacc tcggggccgc ccactctcag cctcccaacc ctctctgcct 2160
cagcgggcaa caggcgatgg ctctcctggg cgtaagggat caggaagtga gcggctgcct 2220
ccctcagggc tcctggccaa acctccaagg acagcccagc cccccaggcc accagtgcct 2280
gagccagcca caccccgggg tctccagctt tctgccaaca tgtaa 2325

<210> 3
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:amplification
primer

<400> 3
cagccatgga ggcagagcag cggc 24

<210> 4
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:amplification primer

<400> 4
ggaggagatc tttcacatga catacgac 28

<210> 5
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:amplification primer

<400> 5
agtaggatcc atcggtgagg cgtg 24

<210> 6
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:amplification primer

<400> 6
ttacatgttg gcagaaagct ggagacc 27

<210> 7
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:degenerate amplification primer

<220>
<221> modified_base
<222> (24)
<223> n = g, a, c or t

<400> 7
tggaggaga tcttycayat gacntayga 29

<210> 8
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:degenerate amplification primer

<220>
<221> modified_base
<222> (16)
<223> n = g, a, c or t

<220>
<221> modified_base
<222> (25)
<223> n = g, a, c or t

<400> 8
cgtctcgaat gcccknckca tcatngg 27

<210> 9
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:first round 5' RACE gene specific primer

<400> 9
cctgctgccc atagccaatg cacagc 26

<210> 10
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:second round nested 5' RACE gene specific primer

<400> 10
gcaccacgaa ctgcagacag ccatc 25

<210> 11
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nested 3' RACE gene specific reamplification primer

<400> 11
gttctcacca agctgcgctt tgaggt 27

<210> 12
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nested 3' RACE
gene specific primer

<400> 12
ccagcatggg ctgctcagtg tgctg 25

<210> 13
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nested 3' RACE
gene specific primer

<400> 13
gcccactctc agcctcccaa ccctc 25

<210> 14
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:nested 3' RACE
gene specific primer

<400> 14
cccaaccaag cttgcctcag cgggcaacag gcgatgg 37

<210> 15
<211> 875
<212> PRT
<213> Homo sapiens

<220>
<223> human hyperpolarization-activated voltage-gated
cation channel 1 (HAC1)

<400> 15
Met Asp Ala Arg Gly Gly Gly Gly Arg Pro Gly Glu Ser Pro Gly Ala
1 5 10 15

Thr Pro Ala Pro Gly Pro Pro Pro Pro Pro Pro Ala Pro Pro Pro Gly
20 25 30

Pro Gly Pro Ala Pro Pro Gln His Pro Pro Arg Ala Glu Ala Leu Pro
35 40 45

Pro Glu Ala Ala Asp Glu Gly Gly Pro Arg Gly Arg Leu Arg Ser Arg
50 55 60

Asp Ser Ser Cys Gly Arg Pro Gly Thr Pro Gly Ala Ala Ser Thr Ala
65 70 75 80

Lys Gly Ser Pro Asn Gly Glu Cys Gly Arg Gly Glu Pro Gln Cys Ser
85 90 95

```
Pro Ala Gly Pro Glu Gly Pro Ala Arg Gly Pro Lys Val Ser Phe Ser
            100                 105                 110

Cys Arg Gly Ala Ala Ser Gly Pro Ala Pro Gly Pro Gly Pro Ala Glu
        115                 120                 125

Glu Ala Gly Ser Glu Glu Ala Gly Pro Ala Gly Glu Pro Arg Gly Ser
    130                 135                 140

Gln Ala Ser Phe Met Gln Arg Gln Phe Gly Ala Leu Leu Gln Pro Gly
145                 150                 155                 160

Val Asn Lys Phe Ser Leu Arg Met Phe Gly Ser Gln Lys Ala Val Glu
                165                 170                 175

Arg Glu Gln Glu Arg Val Lys Ser Ala Gly Ala Trp Ile Ile His Pro
            180                 185                 190

Tyr Ser Asp Phe Arg Phe Tyr Trp Asp Phe Thr Met Leu Leu Phe Met
        195                 200                 205

Val Gly Asn Leu Ile Ile Ile Pro Val Gly Ile Thr Phe Phe Lys Asp
    210                 215                 220

Glu Thr Thr Ala Pro Trp Ile Val Phe Asn Val Val Ser Asp Thr Phe
225                 230                 235                 240

Phe Leu Met Asp Leu Val Leu Asn Phe Arg Thr Gly Ile Val Ile Glu
                245                 250                 255

Asp Asn Thr Glu Ile Ile Leu Asp Pro Glu Lys Ile Lys Lys Lys Tyr
            260                 265                 270

Leu Arg Thr Trp Phe Val Val Asp Phe Val Ser Ser Ile Pro Val Asp
        275                 280                 285

Tyr Ile Phe Leu Ile Val Glu Lys Gly Ile Asp Ser Glu Val Tyr Lys
    290                 295                 300

Thr Ala Arg Ala Leu Arg Ile Val Arg Phe Thr Lys Ile Leu Ser Leu
305                 310                 315                 320

Leu Arg Leu Leu Arg Leu Ser Arg Leu Ile Arg Tyr Ile His Gln Trp
                325                 330                 335

Glu Glu Ile Phe His Met Thr Tyr Asp Leu Ala Ser Ala Val Met Arg
            340                 345                 350

Ile Cys Asn Leu Ile Ser Met Met Leu Leu Leu Cys His Trp Asp Phe
        355                 360                 365

Cys Leu Gln Phe Leu Val Pro Met Leu Gln Asp Phe Pro Arg Asn Cys
    370                 375                 380

Trp Val Ser Ile Asn Gly Met Val Asn His Ser Trp Ser Glu Leu Tyr
385                 390                 395                 400

Ser Phe Ala Leu Phe Lys Ala Met Ser His Met Leu Cys Ile Gly Tyr
                405                 410                 415
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Gly Arg Gln Ala Pro Glu Ser Met Thr Asp Ile Trp Leu Thr Met Leu
420 425 430

Ser Met Ile Val Gly Ala Thr Cys Tyr Ala Met Phe Ile Gly His Ala
435 440 445

Thr Ala Leu Ile Gln Ser Leu Asp Ser Ser Arg Arg Gln Tyr Gln Glu
450 455 460

Lys Tyr Lys Gln Val Glu Gln Tyr Met Ser Phe His Lys Leu Pro Ala
465 470 475 480

Asp Phe Arg Gln Lys Ile His Asp Tyr Tyr Glu His Arg Tyr Gln Gly
485 490 495

Lys Met Phe Asp Glu Asp Ser Ile Leu Gly Glu Leu Asn Gly Pro Leu
500 505 510

Arg Glu Glu Ile Val Asn Phe Asn Cys Arg Lys Leu Val Ala Ser Met
515 520 525

Pro Leu Phe Ala Asn Ala Asp Pro Asn Phe Val Thr Ala Met Leu Thr
530 535 540

Lys Leu Lys Phe Glu Val Phe Gln Pro Gly Asp Tyr Ile Ile Arg Glu
545 550 555 560

Gly Thr Ile Gly Lys Lys Met Tyr Phe Ile Glx His Gly Val Val Ser
565 570 575

Val Leu Thr Lys Gly Asn Lys Glu Met Lys Leu Ser Asp Gly Ser Tyr
580 585 590

Phe Gly Glu Ile Cys Leu Leu Thr Arg Gly Arg Arg Thr Ala Ser Val
595 600 605

Arg Ala Asp Thr Tyr Cys Arg Leu Tyr Ser Leu Ser Val Asp Asn Phe
610 615 620

Asn Glu Val Leu Glu Glu Tyr Pro Met Met Arg Arg Ala Phe Glu Thr
625 630 635 640

Val Ala Ile Asp Arg Leu Asp Arg Ile Gly Lys Lys Asn Ser Ile Leu
645 650 655

Leu His Lys Val Gln His Asp Leu Asn Ser Gly Val Phe Asn Asn Gln
660 665 670

Glu Asn Ala Ile Ile Gln Glu Ile Val Lys Tyr Asp Arg Glu Met Val
675 680 685

Gln Gln Ala Glu Leu Gly Gln Arg Val Gly Leu Phe Pro Pro Pro Pro
690 695 700

Pro Pro Pro Gln Val Thr Ser Ala Ile Ala Thr Leu Gln Gln Ala Ala
705 710 715 720

Ala Met Ser Phe Cys Pro Gln Val Ala Arg Pro Leu Val Gly Pro Leu
725 730 735

Ala Leu Gly Ser Pro Arg Leu Val Arg Arg Pro Pro Pro Gly Pro Ala
740 745 750

Pro Ala Ala Ala Ser Pro Gly Pro Pro Pro Pro Ala Ser Pro Pro Gly
755 760 765

Ala Pro Ala Ser Pro Arg Ala Pro Arg Thr Ser Pro Tyr Gly Gly Leu
770 775 780

Pro Ala Ala Pro Leu Ala Gly Pro Ala Leu Pro Ala Arg Arg Leu Ser
785 790 795 800

Arg Ala Ser Arg Pro Leu Ser Ala Ser Gln Pro Ser Leu Pro His Gly
805 810 815

Ala Pro Gly Pro Ala Ala Ser Thr Arg Pro Ala Ser Ser Ser Thr Pro
820 825 830

Arg Leu Gly Pro Thr Pro Ala Ala Arg Ala Ala Ala Pro Ser Pro Asp
835 840 845

Arg Arg Asp Ser Ala Ser Pro Gly Ala Ala Gly Gly Leu Asp Pro Gln
850 855 860

Asp Ser Ala Arg Ser Arg Leu Ser Ser Asn Leu
865 870 875

<210> 16
<211> 749
<212> PRT
<213> Homo sapiens

<220>
<223> human hyperpolarization-activated voltage-gated cation channel 2 (HAC2) missing amino terminus

<400> 16
Lys Glu Gln Glu Arg Val Lys Thr Ala Gly Phe Trp Ile Ile His Pro
1 5 10 15

Tyr Ser Asp Phe Arg Phe Tyr Trp Asp Leu Ile Met Leu Ile Met Met
20 25 30

Val Gly Asn Leu Val Ile Ile Pro Val Gly Ile Thr Phe Phe Thr Glu
35 40 45

Gln Thr Thr Thr Pro Trp Ile Ile Phe Asn Val Ala Ser Asp Thr Val
50 55 60

Phe Leu Leu Asp Leu Ile Met Asn Phe Arg Thr Gly Thr Val Asn Glu
65 70 75 80

Asp Ser Ser Glu Ile Ile Leu Asp Pro Lys Val Ile Lys Met Asn Tyr
85 90 95

Leu Lys Ser Trp Phe Val Val Asp Phe Ile Ser Ser Ile Pro Val Asp
100 105 110

Tyr Ile Phe Leu Ile Val Glu Lys Gly Met Asp Ser Glu Val Tyr Lys
115 120 125

Thr Ala Arg Ala Leu Arg Ile Val Arg Phe Thr Lys Ile Leu Ser Leu
130 135 140

Leu Arg Leu Leu Arg Leu Ser Arg Leu Ile Arg Tyr Ile His Gln Trp
145 150 155 160

Glu Glu Ile Phe His Met Thr Tyr Asp Leu Ala Ser Ala Val Val Arg
165 170 175

Ile Phe Asn Leu Ile Gly Met Met Leu Leu Leu Cys His Trp Asp Phe
180 185 190

Cys Leu Gln Phe Leu Val Pro Leu Leu Gln Asp Phe Pro Pro Asp Cys
195 200 205

Trp Val Ser Leu Asn Glu Met Val Asn Asp Ser Trp Gly Lys Gln Tyr
210 215 220

Ser Tyr Ala Leu Phe Lys Ala Met Ser His Met Leu Cys Ile Gly Tyr
225 230 235 240

Gly Ala Gln Ala Pro Val Ser Met Ser Asp Leu Trp Ile Thr Met Leu
245 250 255

Ser Met Ile Val Gly Ala Thr Cys Tyr Ala Met Phe Val Gly His Ala
260 265 270

Thr Ala Leu Ile Gln Ser Leu Asp Ser Ser Arg Arg Gln Tyr Gln Glu
275 280 285

Lys Tyr Lys Gln Val Glu Gln Tyr Met Ser Phe His Lys Leu Pro Ala
290 295 300

Asp Met Arg Gln Lys Ile His Asp Tyr Tyr Glu His Arg Tyr Gln Gly
305 310 315 320

Lys Ile Phe Asp Glu Glu Asn Ile Leu Asn Glu Leu Asn Asp Pro Leu
325 330 335

Arg Glu Glu Ile Val Asn Phe Asn Cys Arg Lys Leu Val Ala Thr Met
340 345 350

Pro Leu Phe Ala Asn Ala Asp Pro Asn Phe Val Thr Ala Met Leu Ser
355 360 365

Lys Leu Arg Phe Glu Val Phe Gln Pro Gly Asp Tyr Ile Ile Arg Glu
370 375 380

Gly Ala Val Gly Lys Lys Met Tyr Phe Ile Glx His Gly Val Ala Gly
385 390 395 400

Val Ile Thr Lys Ser Ser Lys Glu Met Lys Leu Thr Asp Gly Ser Tyr
405 410 415

Phe Gly Glu Ile Cys Leu Leu Thr Lys Gly Arg Arg Thr Ala Ser Val
420 425 430

Arg Ala Asp Thr Tyr Cys Arg Leu Tyr Ser Leu Ser Val Asp Asn Phe
435 440 445

Asn Glu Val Leu Glu Glu Tyr Pro Met Met Arg Arg Ala Phe Glu Thr
450 455 460

Val Ala Ile Asp Arg Leu Asp Arg Ile Gly Lys Lys Asn Ser Ile Leu
465 470 475 480

Leu Gln Lys Phe Gln Lys Asp Leu Asn Thr Gly Val Phe Asn Asn Gln
485 490 495

Glu Asn Glu Ile Leu Lys Gln Ile Val Lys His Asp Arg Glu Met Val
500 505 510

Gln Ala Ile Ala Pro Ile Asn Tyr Pro Gln Met Thr Thr Leu Asn Ser
515 520 525

Thr Ser Ser Thr Thr Thr Pro Thr Ser Arg Met Arg Thr Gln Ser Pro
530 535 540

Pro Val Tyr Thr Ala Thr Ser Leu Ser His Ser Asn Leu His Ser Pro
545 550 555 560

Ser Pro Ser Thr Gln Thr Pro Gln Pro Ser Ala Ile Leu Ser Pro Cys
565 570 575

Ser Tyr Thr Thr Ala Val Cys Ser Pro Pro Val Gln Ser Pro Leu Ala
580 585 590

Ala Arg Thr Phe His Tyr Ala Ser Pro Thr Ala Ser Gln Leu Ser Leu
595 600 605

Met Gln Gln Gln Pro Gln Gln Gln Val Gln Gln Ser Gln Pro Pro Gln
610 615 620

Arg Gln Pro Gln Gln Pro Ser Pro Gln Pro Gln Thr Pro Gly Ser Ser
625 630 635 640

Thr Pro Lys Asn Glu Val His Lys Ser Thr Gln Ala Leu His Asn Thr
645 650 655

Asn Leu Thr Arg Glu Val Arg Pro Phe Ser Ala Trp Gln Pro Ser Leu
660 665 670

Pro His Glu Val Ser Thr Leu Ile Ser Arg Pro His Pro Thr Val Gly
675 680 685

Glu Ser Leu Ala Ser Ile Pro Gln Pro Val Thr Ala Val Pro Gly Thr
690 695 700

Gly Leu Gln Ala Gly Gly Arg Ser Thr Val Pro Gln Arg Val Thr Phe
705 710 715 720

Phe Arg Gln Met Ser Ser Gly Ala Ile Pro Pro Asn Arg Gly Val Leu
725 730 735

Pro Ala Pro Leu Pro Leu Ile Thr Pro His Pro Lys Lys
740 745